

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 19:03:46 ; Search time 14.4462 Seconds
(without alignments)
733.219 Million cell updates/sec

Title: US-09-719-748-2

Perfect score: 1846

Sequence: 1 MEPRKQKVEDFDYDGEELG.....TEEDARKKALHRRRSTSS 360

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
1: /cgnt2_6/prodata/1/1aa/5A_COMB.pep.*
2: /cgnt2_6/prodata/1/1aa/5B_COMB.pep.*
3: /cgnt2_6/prodata/1/1aa/6A_COMB.pep.*
4: /cgnt2_6/prodata/1/1aa/6B_COMB.pep.*
5: /cgnt2_6/prodata/1/1aa/PCTUS_COMB.pep.*
6: /cgnt2_6/prodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1248	67.6	1423	4 US-08-810-712-10	Sequence 10, Appl
2	1239.5	67.1	331	4 US-08-810-712-24	Sequence 24, Appl
3	1166	63.2	454	2 US-09-159-385-1	Sequence 1, Appl
4	1166	63.2	454	4 US-09-186-277-1	Sequence 1, Appl
5	1140	61.8	448	2 US-09-159-385-2	Sequence 2, Appl
6	1140	61.8	448	4 US-09-186-277-2	Sequence 2, Appl
7	761	41.2	160	3 US-09-221-235-11	Sequence 11, Appl
8	761	41.2	160	3 US-09-221-928-11	Sequence 11, Appl
9	761	41.2	160	3 US-09-221-527-11	Sequence 11, Appl
10	761	41.2	160	4 US-09-221-336-11	Sequence 11, Appl
11	761	41.2	160	4 US-09-221-416-11	Sequence 11, Appl
12	761	41.2	160	4 US-09-221-245-11	Sequence 11, Appl
13	761	41.2	160	4 US-09-163-115-11	Sequence 11, Appl
14	761	41.2	160	4 US-09-221-528-11	Sequence 11, Appl
15	761	41.2	160	4 US-09-593-553-11	Sequence 11, Appl
16	761	41.2	160	4 US-09-221-337-11	Sequence 11, Appl
17	654	35.4	260	2 US-07-857-224B-23	Sequence 23, Appl
18	571.5	31.0	261	2 US-07-857-224B-22	Sequence 22, Appl
19	564.5	30.6	307	1 US-08-713-828-1	Sequence 1, Appl
20	564.5	30.6	307	2 US-08-919-627-1	Sequence 1, Appl
21	564.5	30.6	307	2 US-09-096-245-1	Sequence 1, Appl
22	530.5	28.7	370	2 US-08-878-989-19	Sequence 19, Appl
23	530.5	28.7	370	4 US-09-272-796-19	Sequence 19, Appl
24	530.5	28.7	370	4 US-09-457-040B-31	Sequence 31, Appl
25	508	27.5	2860	2 US-08-826-267-2	Sequence 2, Appl
26	507.5	27.5	556	4 US-09-800-960-4	Sequence 4, Appl
27	507	27.5	343	2 US-08-878-989-5	Sequence 5, Appl

28	507	27.5	343	4 US-09-272-796-5	Sequence 5, Appl
29	501	27.1	565	4 US-09-800-960-2	Sequence 2, Appl
30	499	27.0	424	2 US-08-715-568A-1	Sequence 1, Appl
31	490	26.5	295	1 US-07-951-715A-23	Sequence 23, Appl
32	490	26.5	295	2 US-08-459-448A-23	Sequence 23, Appl
33	490	26.5	295	3 US-08-459-595A-23	Sequence 23, Appl
34	490	26.5	295	3 US-08-459-504B-23	Sequence 23, Appl
35	490	26.5	295	3 US-08-459-444-23	Sequence 23, Appl
36	490	26.5	295	4 US-09-547-422-23	Sequence 23, Appl
37	477.5	25.9	463	1 US-07-951-715A-25	Sequence 25, Appl
38	477.5	25.9	463	2 US-08-459-448A-25	Sequence 25, Appl
39	477.5	25.9	463	3 US-08-459-595A-25	Sequence 25, Appl
40	477.5	25.9	463	3 US-08-459-504B-25	Sequence 25, Appl
41	477.5	25.9	463	3 US-08-459-444-25	Sequence 0, Appl
42	477.5	25.9	463	4 US-09-547-422-25	Sequence 0, Appl
43	476	25.8	264	2 US-07-857-224B-18	Sequence 18, Appl
44	474	25.7	264	2 US-07-857-224B-24	Sequence 24, Appl
45	470.5	25.5	520	4 US-09-257-825B-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-810-712-10
; Sequence 10, Application US/08810712G
; Patent No. 6160106
; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Co. Ltd
; TITLE OF INVENTION: Tumor Suppressor Genes, Proteins Encoded Thereby and
; FILE REFERENCE: sequence list
; CURRENT FILING DATE: 1997-03-03
; EARLIER APPLICATION NUMBER: PCT/US94/11598
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1423
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-810-712-10

Query Match 67.6% Score 1248; DB 4; Length 1423;

Best Local Similarity 66.5% Pred. No. 4.3e-100; Matches 236; Conservative 60; Mismatches 43; Indels 16; Gaps 3;

QY	1	MEPRKQKVEDFDYDGEELGSGQFAIVKCKEKSGLFYAKFKKRSRARSRCVSRRE	60
DB	1	MTVFRQENVDDYDYGEEELSGQFAVVKCKEKSGLQYPAKFKKRTKSSRRGVSRRE	60
QY	61	IEREVSILRQHLHNVTLDHVDYENRTDVVILDELVSGETLFDPLAKESLSEEEATSF	120
DB	61	IEREVSILKQHPVITLHEVYENKTDVILDELVSAGELFDPLAKESLSEEEATFEL	120
QY	121	KQILDGVNLTHTKIAHFDLKPENIMLDKNIPPHIKLIDPLGAHETEDGVEKKNIGT	180
DB	121	KQILNGVYVLTSLQIAHFDLKPENIMLDKNIPPHIKLIDPLGAHETEDGVEKKNIGT	172
QY	181	PEFAPELVNTEPGLGELDMWSIGVITYILSGASPFGLDTRKQETLANVSAVNEEED	240
DB	173	PEFAPELVNTEPGLGELDMWSIGVITYILSGASPFGLDTRKQETLANVSAVNEEED	232
QY	241	FSHTSELKDFIRKLIVETRRRLITIOBALRHPWTPVDNOQAMVRSVNLNFRQY	300
DB	233	FSNLSALAKDFIRRLVAVDPKKRMITQDSLOHPWTKRPDQOALSRSKSAVMEKFKFA	292
QY	301	VRRRKVSFSVSLCNHLTRSLMKVHL---RPDELRNCSDEEDTARRKALH	352
DB	293	ARKWKQSVRLISLCQRLSRFSLSRNSMVSARSDDTL---DEEDSFVMAIIH	342


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: Patent NO. 5180358
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: GENERAL INFORMATION:
: APPLICANT: Acton, Susan
: TITLE OF INVENTION: NOVEL CSAPk-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
: FILE REFERENCE: NMI-050
: CURRENT APPLICATION NUMBER: US/09/221,245
: CURRENT FILING DATE: 1998-12-26
: EARLIER APPLICATION NUMBER: US 09/163,115
: EARLIER FILING DATE: 1998-09-29
: NUMBER OF SEQ. ID NOS: 15
: SOFTWARE: PatentIn Ver. 2.0
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: SEQ ID NO 11
:
: LENGTH: 160
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: TYPE: PRT
:
: ORGANISM: Homo sapiens
:
: US-09-221-245-11

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Best Local Similarity	94.38;	Pred. NO. 5.6e-59;		
Matches 150; Conservative	4;	Mismatches 3;	Indels 2;	Gaps 1;

[illegible]

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RESULT 13
US-09-163-115-11
: Sequence 11, Application US/09163115A
: Patent No. 6183962
: GENERAL INFORMATION:
: APPLICANT: Acton, Susan
: TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
: FILE REFERENCE: NMT-050
: CURRENT APPLICATION NUMBER: US/09/163,115A
: CURRENT FILING DATE: 1998-09-29
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 11
: LENGTH: 160
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-163-115-11

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QY	202	SIGVITVLLSSASPLGDTKOETLANITSVSYDDEEEFSHTSELAKDFIKRLVKEPR	261	
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Db	4	SLSYV--LSLSASPFLOGTKEITLANITAVSYDDEEFSQTSSELAKFIKRLVKEIR	61	
QY	262	KRLTIOEALRHFWITPVYDNOQAMVRRESVYVLENFRKOYVRRRWKLSFISVSLCNHLTRS	321	
Db	62	KRLTIOEALRHFWITPVYDNOQAMVRRESVYVLENFRKOYVRRRWKLSFISVSLCNHLTRS	121	
QY	362	LMKKVHLRPDEDLRNCESTDEEDIAARKKALHRRRSSTS	360	
Db	122	LMKKVHLRPDEDLRNCESTDEEDIAARKKALHRRRSSTS	160	

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; Sequence 11, Application US/09221528
; Patent No. 6190874

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? GENERAL INFORMATION:
? APPLICANT: Acton, Susan
? TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
? FILE REFERENCE: MNI-050
? CURRENT APPLICATION NUMBER: US/09/221,528
? CURRENT FILING DATE: 1998-12-28
? EARLIER APPLICATION NUMBER: 09/163,115
? EARLIER FILING DATE: 1998-09-29
? NUMBER OF SEQ. ID NOS.: 15
? SOFTWARE: Patentln Ver. 2.0
? SEQ ID NO 11
? LENGTH: 160
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-09-221-528-11

Query Match          41.2%   Score 761; DB 4; Length 160;
Best Local Similarity 94.3%   Pred. No. 5,6e-59;
Matches 150; Conservative 4; Mismatches 3; Indels 2; Gaps

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Query Match	41.2%	Score 761	DB 4	Length 160
Best Local Similarity	94.3%	Pred. 0.5, 6e-59		
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			Gaps	1
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4	SLSYV--LTLSSASFLGDTKEQTANTITAVSYDDPEEFSTSLADFIKLLYKETR	61		

QY	262	KRLTIOEALRHPWITTPVDNOCAMVRRSSVNLLENFRQYARRRKLKSFSTVSLCNHLTRS	321
Db	62	KRLTIOEALRHPWITTPVDNOCAMVRRSSVNLLENFRQYARRRKLKSFSTVSLCNHLTRS	121
QY	322	LMKKVHLRPDDDLRNCESDTRFEDDLARRKALHPRRRSSTS	360
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RESULT 15
US-09-593-553-11
: Sequence 11, Application US/09593553
: Patent No. 6200770
: GENERAL INFORMATION:
: APPLICANT: Acton, Susan
: TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
: FILE REFERENCE: MNI-050
: CURRENT APPLICATION NUMBER: US/09/593,553
: CURRENT FILING DATE: 2000-06-14
: PRIOR APPLICATION NUMBER: 09/163,115
: PRIOR FILING DATE: 1998-09-28
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 11
: LENGTH: 160
: type: prt
: ORGANISM: Homo sapiens
: US-09-593-553-11

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Query Match	41.2%;	Score 761;	DB 4;	length 160;
Best Local Similarity	94.3%;	Pred. No. 5.6e-59;		
Matches	150;	Conservative	4;	Mismatches 3; Indels 2; Gaps 1;
QY	202	SGVITVYLLSGASPFELGDTKQETLANITVSVDDEEFHSHTSELANDFIRKLIVKETR	261	
Db	4	SLSVY--LTLSGASPFELGDTKQETLANITVAISYDDEEFSGTSELANDFIRKLIVKETR	61	
QY	262	KRLTIQELRRPWITPVVNOQAMVARESEVNLLENRKQIVRRRKLSTSIYSLCNHLTRS	321	
Db	62	KRLTIQELRRPWITPVVNOQAMVARESEVNLLENRKQIVRRRKLSTSIYSLCNHLTRS	121	
QY	322	LMKKVHLRRPDEDLRNCESDTEEDLARRKALHPRRRSSTS	360	
Db	122	LMKKVHLRRPDEDLRNCESDTEEDLARRKALHPRRRSSTS	160	

Search completed: March 26, 2003, 19:11:21
Job time : 15.4462 secs

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GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 19:10:26 ; Search time 15.0241 Seconds

(without alignments)
1407.110 Million cell updates/sec

Title: US-09-719-748-2

Perfect score: 1846

Sequence: 1 MEPPKQKQVEDFYDIGELG.....TEEDLARKALHPRRSSTS 360

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 237916 seqs, 58723674 residues

Total number of hits satisfying chosen parameters: 237916

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/PCCTIS_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1166	63.2	454	10	US-09-771-161A-238
2	761	41.2	160	10	US-09-757-982-11
3	677.5	36.7	298	10	US-09-858-664A-17
4	664.5	36.0	508	10	US-09-858-664A-18
5	639.5	34.6	839	10	US-09-925-300-1442
6	633.5	34.3	388	10	US-09-940-921B-7
7	633.5	34.3	398	10	US-09-940-921B-9
8	603.5	32.7	596	10	US-09-797-039-8
9	564	30.6	357	9	US-10-024-036B-2
10	543.5	29.4	460	9	US-09-935-464-3
11	543.5	29.4	476	9	US-09-935-464-5
12	541	29.3	26926	9	US-09-759-508B-2
13	530.5	28.7	370	9	US-10-142-356-7
14	530.5	28.7	370	10	US-09-817-181-4
15	530.5	28.7	846	10	US-09-858-664A-3
16	530	28.7	317	9	US-09-935-464-36
17	526	28.5	549	10	US-09-858-664A-5
18	512	27.7	414	10	US-09-858-664A-13
19	507.5	27.5	556	12	US-10-096-960-4

20	501	27.1	565	12	US-10-096-960-2	Sequence 2, Appli
21	500	27.1	274	10	US-09-858-664A-14	Sequence 14, Appli
22	499.5	27.1	648	9	US-10-024-036B-5	Sequence 5, Appli
23	499.5	27.1	817	10	US-09-992-481-4	Sequence 23, Appli
24	490	26.5	295	9	US-09-988-462-23	Sequence 887, App
25	483	26.2	416	9	US-09-925-299-887	Sequence 25, Appli
26	483	26.2	416	10	US-09-988-462-25	Sequence 39, Appli
27	477.5	25.9	549	10	US-09-828-313-39	Sequence 17, Appli
28	475.5	25.8	406	10	US-09-771-161A-210	Sequence 2, Appli
29	472.5	25.6	639	10	US-09-854-731-17	Sequence 10, App
30	470.5	25.5	326	10	US-09-817-181-2	Sequence 4, Appli
31	470	25.5	623	10	US-09-854-731-4	Sequence 18, Appli
32	468.5	25.4	625	10	US-09-854-731-18	Sequence 2, Appli
33	468.5	25.4	1665	10	US-09-858-664A-2	Sequence 2, Appli
34	467.5	25.3	2630	9	US-10-077-130-2	Sequence 2, Appli
35	467.5	25.3	7968	9	US-10-077-130-5	Sequence 5, Appli
36	467.5	25.3	7968	10	US-09-797-039-2	Sequence 2, Appli
37	466.5	25.3	501	10	US-10-153-921-2	Sequence 2, Appli
38	466.5	25.3	385	9	US-10-116-332-2	Sequence 4, Appli
39	465	25.2	765	9	US-10-217-357-4	Sequence 4, Appli
40	458.5	24.8	765	10	US-09-975-326-4	Sequence 2, Appli
41	458.5	24.8	766	9	US-09-934-406-2	Sequence 4, Appli
42	458.5	24.8	766	9	US-10-217-357-2	Sequence 2, Appli
43	458.5	24.8	766	10	US-09-975-326-2	Sequence 2, Appli
44	458.5	24.8	464	9	US-09-988-462-22	Sequence 22, Appli
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ALIGNMENTS

RESULT 1
US-09-771-161A-238
Sequence 238, Application US/09771161A
Patent No. US20020110811A1
GENERAL INFORMATION:
APPLICANT: LEVINE, et al
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 136776
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
SOFTWARE: PatentIn version 3.0
SEQ ID NO 238
LENGTH: 454
TYPE: PRT
ORGANISM: Homo sapiens
US-09-771-161A-238

Query Match 63.2%; Score 1166; DB 10; Length 454;
Best Local Similarity 64.7%; Pred. No. 2.9e-77;
Matches 233; Conservative 49; Mismatches 60; Indels 18; Gaps 3;

QY 1 MEPPKQKQVEDFYDIGELGSGGFATYKKCKREKSTGEVAAKFTKKRQSRASRGVSREE 60
DB 1 MSTRFQEDVDYHKEGELSGGFATYKKCKRQGTGKETAATIKKRLSSRRGVSREE 60

QY IEREVSLRQVLTTHNVYTTLDVYENKRTDVVHILEVSGELFDFLQAKESLSEEAFTSPT 120
DB IEREVSLRQVLTTHNVYTTLDVYENKRTDVVHILEVSGELFDFLQAKESLSEEAFTSPT 120

QY 121 KQLDGVNYLHTKRIKIAFDLKPENIMLDKNIPFPHKLDELGLAHEIEGVCFKNTFCT 180
DB 121 KQLDGVNYLHTKRIKIAFDLKPENIMLDKNVNPRIKLIDFSAHKIEAGNFKNFCT 180

QY 181 PEVAVPEIYVEPLGSEADWMSIGVITYTLLSGASPLGDTKQETLANITSVSKDFDEEF 240
DB 181 PEVAVPEIYVEPLGSEADWMSIGVITYTLLSGASPLGDTKQETLANITSVSKDFDEEF 240

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Db 181 PEVAPETVNEPLGLEADMSIGVITYLLSGASPFGLGTQOETLNLISAVNDFDEY 240
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Db 241 FSHTSGLADFTKRLKYTKRKLITQELRHPWITPVNOQAMVRESVNLNFRKQY 293
Qy 301 VRRRWLSLSISLCLNHLRSLMKVHLRDE--DLRNCESDTEEDIAARRKALHPRRS 357
Db 294 RRLKLTIRLKEYTKSHS-----LPPNNSYADFEFRFSKYLEEAAAEGLRELDORS 345

RESULT 2
US-09-757-982-11
; Sequence 11, Application US/09757982
; Patent No. US20020094559A1
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-050
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 09/163,115
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-757-982-11

Query Match 41.2%; Score 761; DB 10; Length 160;
Best Local Similarity 94.3%; Pred. No. 2,1e-48;
Matches 150; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

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Db 4 SLSTV--LTLGASPFGLGTQOETLNLITAVSYDFDEFSQSLKAKDFTKRLKYETR 61
Qy 262 KRLTQELRHPWITPVNOQAMVRESVNLNFRKQYVRRWKLSPSIVSLCNHLTRS 321
Db 62 KRLTQELRHPWITPVNOQAMVRESVNLNFRKQYVRRWKLSPSIVSLCNHLTRS 121
Qy 322 LMKVHLRPDEDLRNCESDTEEDIAARRKALHPRRSSTS 360
Db 122 LMKVHLRPDEDLRNCESDTEEDIAARRKALHPRRSSTS 160

RESULT 3
US-09-858-664A-17
; Sequence 17, Application US/09858664A
; Patent No. US20020072491A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui, et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO00927-CIP
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/711,134
; PRIOR FILING DATE: 2000-11-11
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-858-664A-17

Query Match 36.7%; Score 677.5; DB 10; Length 298;
Best Local Similarity 45.0%; Pred. No. 4.9e-42;
Matches 136; Conservative 56; Mismatches 95; Indels 15; Gaps 5;

```

```

Qy 7 QKVEDFYDIGEELSGQFAIVKCKREKSTGLEAYAKFKKQSRASRGVSRREIEREV 66
Db 1 QKVEDFYDIGEELSGQFAIVKCKREKSTGLEAYAKFKKQSRASRGVSRREIEREV 54
Qy 67 ILKQVLAHNVITLHDVYENKTDVNHILEVSGGELDFDLQKE-SLSEEAITSFIQIOL 125
Db 55 IMNGLHHPKLVQCVDAFEERKANIVMLVLSGGELFERIIDEDFELTERECIKYMQIIE 114
Qy 126 GVNYLHFKTKLAHFDLKPENIMLDKNIPRIKILIDFGLAHEIDEGVEFNINFGTPEVA 185
Db 115 GVEYIHKQGIIVHDLKPENIMCVNKT--GTRIKLIDFGLARLENNAGSLKVLFGTPEVA 172
Qy 186 PEIVNEPLGLEADMSIGVITYLLSGASPFGLGTQOETLNLISAVNDFDEFSHNS 245
Db 173 PEIVNEPLISATDMMSIGVICYLLVSGLSPFMGDNENETLANVTSATWDFDEAFDEIS 232
Qy 246 ELAKDFTKRLKYTKRKLITQELRHPWITPVNOQAMVRESVNLNFRKQYVRR 304
Db 233 DDAKDFISNLKDKMKRNLDTQCLQHPMLKDKTKMEA-----KLSKDRMKKYMARRK 287
Qy 305 WK 306
Db 288 WQ 289

RESULT 4
US-09-858-664A-18
; Sequence 18, Application US/09858664A
; Patent No. US20020072491A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui, et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO00927-CIP
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/711,134
; PRIOR FILING DATE: 2000-11-11
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-858-664A-18

Query Match 36.0%; Score 664.5; DB 10; Length 508;
Best Local Similarity 48.0%; Pred. No. 8e-41;
Matches 130; Conservative 50; Mismatches 82; Indels 9; Gaps 3;

Qy 6 QKVEDFYDIGEELSGQFAIVKCKREKSTGLEAYAKFKKQSRASRGVSRREIEREV 65
Db 243 EQKVEDFYDIGEELSGQFAIVKCKREKSTGLEAYAKFKKQSRASRGVSRREIEREV 296
Qy 66 SILKQVLAHNVITLHDVYENKTDVNHILEVSGGELDFDLQKE-SLSEEAITSFIQIOL 124
Db 297 SINMCLHHPKLVQCVDAFEERKANIVMLVLSGGELFERIIDEDFELTERECIKYMQIIE 356
Qy 125 DGAVYLTHTKKIAHFDLKPENIMLDKNIPRIKILIDFGLAHEIDEGVEFNINFGTPEV 184
Db 357 EGVEYIHKQGIIVHDLKPENIMCVNKT--GTRIKLIDFGLARLENNAGSLKVLFGTPEV 414
Qy 185 APEIVNEPLGLEADMSIGVITYLLSGASPFGLGTQOETLNLISAVNDFDEFSHNS 244
Db 415 APEIVNEPLISATDMMSIGVICYLLVSGLSPFMGDNENETLANVTSATWDFDEAFDEI 474
Qy 245 SELAKDFTKRLKYTKRKLITQELRHPWITPVNOQAMVRESVNLNFRKQYVRR 275
Db 475 SDAKDFISNLKDKMKRNLDTQCLQHPML 505

```



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RESULT 5
US-09-925-300-1442
: Sequence 1442, Application US/09925300
: Patent No. US20020151681A1
: GENERAL INFORMATION:
: APPLICANT: Craig Rosen,
: APPLICANT: Steve Ruben,
: TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
: FILE REFERENCE: PA101
: CURRENT APPLICATION NUMBER: US/09/925,300
: CURRENT FILING DATE: 2001-08-10
: PRIOR APPLICATION NUMBER: PCT/US00/05988
: PRIOR FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: 60/124,270
: PRIOR FILING DATE: 1999-03-12
: NUMBER OF SEQ ID NOS: 1890
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1442
: LENGTH: 839
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (291)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (295)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (683)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1442

```

```

Query Match          34.6%: Score 639.5; DB: 10; Length 839;
Best Local Similarity 48.3%; Pred. No. 9.3e-39;
Matches 128; Conservative 47; Mismatches 81; Indels 9; Gaps 3;

OY      6 QAKVEDFYDIEELSGGFGAFIVKCKREKSTGLEVAKFIRKRQSHASRGVSREREIEREV 65
       :||| |||| | ||| | : || | :|| | : : || | :
Db8     578 EKKVSDFEDIERLGSGRFGGVFLVEKTKRKVNAGKFFKAYSAR-----EKEINROI 631

OY      66 SILRQLHHNVITLLHDVENRTDVVHILELVSGGELEFDEFLAQE-SLSEEBATSFIKOIL 124
       ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db3     632 SIMMCLNHPRLVQCVDAAPEEKANIAMVLVLSGGELLEFRIDDELTEREXIKYMRQIS 691

OY      125 DGVNLTFRHKTAHNDLKARENIMLDKNIPRIHIKLIDGLAHETDGVEFNINIGTPREV 184
       :||| : : : ||| ||||| : : ||| ||||| : : ||| |||||
Db6     692 EGVEIHHQGVGHIDLKPEENIMCVKT--GTIRIKLIDGLARLRLENMAGSLVLETGPTEPV 749

OY      185 APEIYNVERPLLEDWMSIGVITYTLLSGASPFLGDPTQOEPLANTITSYSTOFDEFESHT 244
       |||:||||| : ||||| ||||| ||||| ||||| : ||||| :
Db5     750 APEIYNVERPIGYARDWMSGIVICYTLVSGLSPPMGDNDETLANVTSATWDFDEAFADEI 809

OY      245 SELAKDFIRKLIVKETRKLITQEA 269
       | : ||||| ||| : : ||| |
Db      810 SDAKDFTISNLKKDKMKNRILDCTHA 834

RESULT 6
US-09-940-921B-7
Sequence 7, Application US/09940921B
Patent NO. US20020147320A1
GENERAL INFORMATION:
APPLICANT: Fiddler, Carl Johan
APPLICANT: Hilburn, Erin
APPLICANT: Nepomniichy, Boris
APPLICANT: Hu, Yi
TITLE OF INVENTION: NO. US20020147320A1el Human Kinase Proteins and Polynucleotides
FILE REFERENCE: LEX-0227-USA
CURRENT APPLICATION NUMBER: US/09/940, 921B
CURRENT FILING DATE: 2002-05-21
PRIORITY APPLICATION NUMBER: US 60/229, 280
PRIOR FILING DATE: 2000-08-31

```

```

: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 7
: LENGTH: 388
: TYPE: PRT
: ORGANISM: homo sapiens
: US-09-940-921b-7

```

	Query Match	34.3%	Score 633.5;	DB 10;	Length 388;	
	Best Local Similarity	45.8%;	Pred. No. 1e-367;			
	Matches 126; Conservative	55;	Mismatches 83;	Indels 11;	Gaps	4
OY	5 KQKVEDFDIDC--BELSGGAPAYKKCEKSTGTLEYAKFTIKROSRASRRCVREEIE	62				
	: : : : : : : : : : :					
Db	96 KOGAVNSFTYSKTTELGGGRGQVHKCEETATGLKLAKIITKTKM-----DKEDVK	149				
OY	63 REVSILROYLHNHVITLHDVENVNRTDVMIILELVSGEELF-D-FLAQEKESI,SEEEAASFTR	121				
	: : : : : : : : : : : : : : :					
Db	150 NEISVMNQDHAHNLIOLYDAFESKNDIVLMVEYVDGEFLDRIDESYMLTDLTPFK	209				
OY	122 QILDGVNLTHTKIAHFDPKLPENIMLLDNIP1PHIKLIDFGSLAEIEDGVEKKNIFFGP	181				
	: : : : : : : : : : :					
Db	210 OICEGIIRHMHWYITLHLDPKLENILCVNND-AKOIKIIDFGIARYYKPREKLKNVFP	267				
OY	162 EVVAPELVNYERPLGLEADMMSTGYTTIIILSCASPPLDGTKOETLANITSVSDPDEEPF	241				
	: : : : : : : : : : : : :					
Db	268 EFLAEVVNVYDFVSEPTDMMSGVAIAYMLLSGLSPFLGNDDETNNIILACRWLDLEDEF	327				
OY	242 SHTSELADFIFKLLVKEFRKRRLTOEQALRHMIT	276				
	: : : : : : : : : : :					
Db	328 ODISEAAEFISKLIKEKSMRISSAEAKHPWLS	362				

```

RESULT 7
US-09-940-921B-9
; Sequence 9, Application US/09940921B
; Patent No. US20020147320A1
GENERAL INFORMATION:
APPLICANT: Fiddle, Carl Johan
APPLICANT: Hilburn, Erin
APPLICANT: Nepomniachy, Boris
APPLICANT: Hu, Yi
TITLE OF INVENTION: No. US20020147320A1el Human Kinase Proteins and Polynucleotides
FILE REFERENCE: LEX-0227-USA
CURRENT APPLICATION NUMBER: US/09/940,921B
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/229,280
PRIOR FILING DATE: 2000-08-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 398
TYPE: PRT
ORGANISM: homo sapiens
US-09-940-921B-9

Query Match          34.3%, Score 633.5, DB 10; Length 398;
Best Local Similarity 45.8%, Pred. No. 1.le=38;
Matches 126; Conservative 55; Mismatches 83; Indels 11; Gaps 4;

OY      5 KQKVEDFYDYG--ELSGGQFAIVKCKREKSTGLEVAAKFLIKRSPASRRGVSRREEIE 62
        || | | | | | | | | | | | | | | | | | | | | | | :||:
Db       96 KGAVNSPYFVSKTEIILGGRGQVHNKCETATGLAKAIIFKTRGM-----DKKEVK 149
        || | | | | | | | | | | | | | | | | | | | | | | :||:

OY      63 REVSLIRQVLHNNVTITLDVYEENKRTDVNHIILELVSGGELP-FLAQKSLSSEEFATSIK 121
        |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      150 NEISVMNDLIDHANLTQLDAFESKNDIIVLMVEYVDGELPRRIDESYNTELDTILPFM 209
        || | | | | | | | | | | | | | | | | | | | | | | :||:

OY     122 QILDENVTLHRKKIAHPPLKRENIMLLDKNPRIPIHKLIIDGLAEHTEDGYEFGNKIFGP 181
        || | | | | | | | | | | | | | | | | | | | | | | :||:
Db     210 QICBSIRHHOMHYLIHDLDKRENILLCVNRD--AKQIKTIIDGLARRVRPREKLKVNFGTP 267
        || | | | | | | | | | | | | | | | | | | | | | | :||:

182 EFVAEINAYNEPLGEADAMMSIGVITYILLGSASPDLGDTFOETLANITSVYDDEEFF 241

```



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Db 141 HRDLKPENLLYLTPREEN---SKIMTDFGLSKMEQNGI--NSTACGTPGVYAPVLAQKPY 196
;
Oy 195 GLEADWMSIGVITYILLSCASPLGDTKQETLANITSVSDFEEFESHSITSELAQDFIRK 254
;
Db 197 SKAVDWSIGVITYILLGCPPEYETESKLFKEIKEGYEFESPPMDDISESAQFICH 256
;
Oy 255 LKVEKTRKRLTQOALRHPMITPVDNOQAVRR--ESVYNLENRKQYVRRRMLSPSIVS 313
;
Db 257 LLEKDNERYTCESKALSHPMI---DGNLTALHRIITPSVSIQ--IQKNFAKSKMQAFNAAA 312
;
Oy 314 LCNHLTRSLMKKVHL-----RPDEDLRNCESDTEE 343
;
Db 313 VVHH-----MRKLHMLHSPGVAPREVENRPPETQASE 344
;

```

```

RESULT 11
US-09-935-464-5
; Sequence 5, Application US/09935464
; Publication No. US20030027153A1
; GENERAL INFORMATION:
; APPLICANT: Meyer, Joanne
; APPLICANT: Barrington-Martin, Rory
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIA
; FILE REFERENCE: 3323/1H702 US1
; CURRENT APPLICATION NUMBER: US/09/935,464
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US 09/757,300
; PRIOR FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-464-5

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Query Match 29.4%; Score 543.5; DB 9; Length 476;
Best Local Similarity 37.1%; Pred. No. 4.4e-32;
Matches 125; Conservative 70; Mismatches 113; Indels 29; Gaps 10;

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```

Oy 17 EELSGOFAIVTKCKREKSTGLEVAAKFIKKROSASRGVSREREVSILROVLHNV 76
;
Db 27 EVLGSASFSEVPLVKORLTKGKLFALKCIK--SPAER---DSLENEIHLVKKIKHENT 80
;
Oy 77 IFLHDVYENRTDVVHILELVSGGELDFDLAOKESLSEEAATSPFIKQILDGVNLTHTKIA 136
;
Db 81 VTLEDIYESTHYLLVMOQLVSGGELDFDLRLENGVYTEKADSLVIOQLASVKKYTLHENGIV 140
;
Oy 137 HFDLKEENIML--DKNIPRPHIKLIDFGLAHEIDEGVEKKNIFGTPPEYAPETIVNTEPL 194
;
Db 141 HRDLKPENLLYLTPREEN---SKIMTDFGLSKMEQNGI--NSTACGTPGVYAPVLAQKPY 196
;
Oy 195 GLEADWMSIGVITYILLSCASPLGDTKQETLANITSVSDFEEFESHSITSELAQDFIRK 254
;
Db 197 SKAVDWSIGVITYILLGCPPEYETESKLFKEIKEGYEFESPPMDDISESAQFICH 256
;
Oy 255 LKVEKTRKRLTQOALRHPMITPVDNOQAVRR--ESVYNLENRKQYVRRRMLSPSIVS 313
;
Db 257 LLEKDNERYTCESKALSHPMI---DGNLTALHRIITPSVSIQ--IQKNFAKSKMQAFNAAA 312
;
Oy 314 LCNHLTRSLMKKVHL-----RPDEDLRNCESDTEE 343
;
Db 313 VVHH-----MRKLHMLHSPGVAPREVENRPPETQASE 344
;

```

```

RESULT 12
US-09-759-508B-2
; Sequence 2, Application US/09759508B
; Publication No. US20020182599A1
; GENERAL INFORMATION:
; APPLICANT: Fishman, Mark C.

```

```

; TITLE OF INVENTION: Methods for Diagnosing and Treating Heart Disease
; FILE REFERENCE: 00766/381002
; CURRENT APPLICATION NUMBER: US/09/759,508B
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/175,787
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 26926
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-508B-2

```

```

Query Match 29.3%; Score 541; DB 9; Length 26926;
Best Local Similarity 38.6%; Pred. No. 7.2e-30;
Matches 102; Conservative 61; Mismatches 91; Indels 10; Gaps 3;

```

```

Oy 13 YDGEELSGOFAIVTKCKREKSTGLEVAAKFIKKROSASRGVSREREVSILROVL 72
;
Db 24754 YMTAEDLGRSEFGLVHRCVETSSKTYMAKFKV-----KGTDOYLVKKESILNIAR 24806
;
Oy 73 HNVITFLHDVYENRTDVVHILELVSGGELDFDLAOKESLSEEAATSPFIKQILDGVNLTHTKIA 131
;
Db 24807 HNVITFLHDVYENRTDVVHILELVSGGELDFDLAOKESLSEEAATSPFIKQILDGVNLTHTKIA 131
;
Oy 132 TKRIAFDLKPENIMLDKNIPRPHIKLIDFGLAHEIDEGVEKKNIFGTPPEYAPETIVNTEPL 191
;
Db 24867 SHNHGFDIPRNPITVOTRRSST--IKIIEGQARQLKPGDNFLLTAAPEYVAPVYVHOH 24924
;
Oy 192 EPLGLEADWMSIGVITYILLSCASPLGDTKQETLANITSVSDFEEFESHSITSELAQDF 251
;
Db 24925 DVSTATDWSLGLTVLVLSGINPLAETMQOITENIMNAEYTFDEAFKEISIEAMD 24984
;
Oy 252 IRKLKVEKTRKRLTQOALRHPMI 275
;
Db 24985 VDRLLVKEKRSMTASALQHPWL 25008
;

```

```

RESULT 13
US-10-142-356-7
; Sequence 7, Application US/10142356
; Publication No. US20030036183A1
; GENERAL INFORMATION:
; APPLICANT: Boylan, John F.
; APPLICANT: Bowers, Alex J.
; TITLE OF INVENTION: Serine-Threonine Kinase Member, h2520-40
; FILE REFERENCE: 01017/37177A
; CURRENT APPLICATION NUMBER: US/10/142,356
; CURRENT FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 60/290,276
; PRIOR FILING DATE: 2001-05-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-142-356-7

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```

Query Match 28.7%; Score 530.5; DB 9; Length 370;
Best Local Similarity 35.7%; Pred. No. 2.9e-31;
Matches 120; Conservative 65; Mismatches 126; Indels 25; Gaps 9;

```

```

Oy 4 FKQ-QKVEDFDYDGEELSGOFAIVTKCKREKSTGLEVAAKFIKKROSASRGVSREREIE 62
;
Db 10 WKQAEIDRDIYDFRDYLGTAFASEVILAEDEKRTQKIVAIAIKIAK--EALKEGES-----SME 64
;
Oy 63 REVSIILROVLHNVITFLHDVYENRTDVVHILELVSGGELDFDLAOKESLSEEAATSPFIKQ 122
;
Db 65 NEIIVLHKIKRPNIVLADDIYESGHLVLLIMQVLSGGELDFDRIYVEKGFYTERDASRLIFQ 124
;
Oy 123 ILDSGVNLTHTKIAHFDLKPENIML--LDKNIPRPHIKLIDFGLAHEIDEGVEKKNIFGT 180
;

```


GenCore version 5.1.4.P5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 19:03:46 ; Search time 10.5538 Seconds
(without alignments) 733.219 Million cell updates/sec

Title: US-09-719-748-2_COPY_13_275

Perfect score: 1343

Sequence: 1 YDIGEELGSGGFALVKKCRE.....LVKTRKRLTIOEALRHPWI 263

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCUUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Length	ID	Description
	1	1121	83.5	454	2	US-09-159-385-1
	2	1121	83.5	454	2	US-09-186-277-1
	3	1106	82.4	448	2	US-09-159-385-2
	4	1106	82.4	448	4	US-09-186-277-2
	5	1079	80.3	331	4	US-08-810-712-24
	6	1079	80.3	1423	4	US-08-810-712-10
	7	649	48.3	260	2	US-07-857-224B-23
	8	571.5	42.6	261	2	US-07-857-224B-22
	9	542.5	40.4	307	1	US-08-713-828-1
	10	542.5	40.4	307	2	US-08-919-627-1
	11	542.5	40.4	307	2	US-09-096-245-1
	12	500	37.2	2860	2	US-08-826-267-2
	13	492.5	36.7	343	4	US-08-878-989-5
	14	492.5	36.7	343	4	US-09-272-796-5
	15	489.5	36.4	424	2	US-08-715-568A-1
	16	485	36.1	370	2	US-08-878-989-19
	17	485	36.1	370	4	US-09-272-796-19
	18	485	36.1	370	4	US-09-457-040B-31
	19	475	35.4	264	2	US-07-857-224B-18
	20	474	35.3	264	2	US-07-857-224B-24
	21	469	34.9	295	1	US-07-951-715A-23
	22	469	34.9	295	2	US-08-459-448A-23
	23	469	34.9	295	3	US-08-459-504B-23
	24	469	34.9	295	3	US-08-459-504B-23
	25	469	34.9	295	3	US-08-459-504B-23
	26	469	34.9	295	4	US-09-547-422-23
	27	469	34.9	556	4	US-09-800-960-4

28	469	34.9	565	4	US-09-800-960-2	Sequence 2, Appl1
29	462	34.4	463	1	US-07-951-715A-25	Sequence 25, Appl1
30	462	34.4	463	2	US-08-459-448A-25	Sequence 25, Appl1
31	462	34.4	463	3	US-08-459-504B-25	Sequence 25, Appl1
32	462	34.4	463	3	US-08-459-504B-25	Sequence 0, Appl1
33	462	34.4	463	3	US-08-459-504B-25	Sequence 0, Appl1
34	462	34.4	463	4	US-07-857-224B-19	Sequence 0, Appl1
35	460	34.3	264	2	US-07-857-224B-19	Sequence 19, Appl1
36	458.5	34.1	456	1	US-08-464-164-2	Sequence 2, Appl1
37	458.5	34.1	456	2	US-08-338-057-2	Sequence 2, Appl1
38	458.5	34.1	456	2	US-08-668-416-2	Sequence 2, Appl1
39	458	34.1	625	4	US-09-347-801-18	Sequence 18, Appl1
40	458	34.1	639	4	US-09-347-801-17	Sequence 17, Appl1
41	457	34.0	623	4	US-09-347-801-4	Sequence 4, Appl1
42	453	33.7	268	2	US-07-857-224B-20	Sequence 20, Appl1
43	448	33.4	387	1	US-08-713-828-3	Sequence 3, Appl1
44	448	33.4	387	2	US-08-919-627-3	Sequence 3, Appl1
45	448	33.4	387	2	US-09-096-245-3	Sequence 3, Appl1

ALIGNMENTS

```
RESULT 1
US-09-159-385-1
; Sequence 1, Application US/09159385
; Patent No. 5958748
; GENERAL INFORMATION:
; APPLICANT: AKIRA, SHIZUO
; APPLICANT: KAMAI, TARO
; TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE
; FILE REFERENCE: PH-569
; CURRENT FILING DATE: 1998-09-23
; EARLIER APPLICATION NUMBER: JP97/261589
; EARLIER FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-159-385-1

Query Match      83.5%; Score 1121; DB 2; Length 454;
Best Local Similarity 79.8%; Pred. No. 3.2e+92;
Matches 210; Conservative 36; Mismatches 17; Indels 0; Gaps 0;

QY 1 YDIGEELGSGGFALVKKCREKSTGLEFAKFKRKRSRSGVSREREIVSLROYL 60
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 13 YDIGEELGSGGFALVKKCKOKGTGKFAKFKRKRLSSRGVSREREIVSLREIR 72
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 61 HHNVITLHVYENRVDVHILELVSGGELEFLAOKESLSEERATSFIRQILDGVNYLHT 120
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 73 HHNVITLHVYENRVDVHILELVSGGELEFLAOKESLSEERATSFIRQILDGVNYLHT 132
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 121 KRIAHFDLPENIMLDKNIPIPIKILDPGLAHEIDCVKRNKIFGTEFVAPELVNTE 180
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 133 KRIAHFDLPENIMLDKNIPIPIKILDPGLAHEIDCVKRNKIFGTEFVAPELVNTE 192
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 181 PLGLEADMSIGITVYILLSGASPFGLDTRKOETLAITSVSDFEDEFSHSELAKDPI 240
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 193 PLGLEADMSIGITVYILLSGASPFGLDTRKOETLAITSVSDFEDEFSHSELAKDPI 252
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 241 RKLIVKTRKRLTIOEALRHPWI 263
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 253 RRLIVKDPKRRMTIAGSLRHSWI 275
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 2
US-09-186-277-1
; Sequence 1, Application US/09186277
; Patent No. 6171841
```

Query Match	82.4%	Score 1106	DB 2	Length 448
Best Local Similarity	79.5%	Pred. No. 6,9e-91		
Matches 209	Conservative 34	Mismatches 20	Indels 0	Gaps
QY	1	YDVGELGGGQFIVAKKCKREKSTGLEVAAKFIKKRQSRASRRCVSREELIREVYSILRQVL	60	
Db	13	YKGGELGGQFIVAKKCKQCGTGMVAAKFIKKRLPSRRRVSREELIREVYSILRIRL	72	
QY	61	HHNVITLHDVYENKRTDVVHLELVSGELFDPLAOKRESSEERATFQIKOILDGVNVILRT	120	

RESULT 5
US-08-810-712-24
Sequence 24, Application US/08810712G
Patent No. 6160106
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co. LTD
TITLE OF INVENTION: Tumor Suppressor Genes, Proteins Encoded Thereby
TITLE OF INVENTION: Use of said Genes and Proteins
FILE REFERENCE: sequencelist
CURRENT APPLICATION NUMBER: US/08/810,712G
CURRENT FILING DATE: 1997-03-03
EARLIER APPLICATION NUMBER: PCT/US94/11598

EARLIER FILING DATE: 1994-10-12
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO: 24
LENGTH: 331
TYPE: PRT
ORGANISM: Homo sapiens
US-08-810-712-24

Query Match 80.3%; Score 1079; DB 4; Length 331;
Best Local Similarity 77.2%; Pred. No. 1.2e-88;
Matches 203; Conservative 39; Mismatches 13; Indels 8; Gaps 1;

OY 1 YDIGELSGGQFAIVKCKREKSTGLEVAAKFTKKRQSRASRGVSREELEREVSILROYL 60
|||
DB 13 YDTGELSGGQFAIVKCKREKSTGLQYPAKFKKRTKSSRGVSREREDEVSILKEIQ 72
OY 61 HHNVITLHDVYENRDTDVHILELVSGGELDFDLAOKESLSEBEATSFIIQIIDGVNYLHT 120
|
DB 73 HPNVITLHEVYENKKTQVILILELVAGGELDFDLAOKESLSEBEATFELKQIINGVYLLHS 132
OY 121 KKAIAFDLKPENIMLLDKNIPPIPHIKLIDFGLAHEIEDGVEPKNIFGTFEFAPELVANE 180
|
DB 133 LQIAHFDLKPENIMLLDRNVKPKRIKIDF-----GNEPKNIFGTFEFAPELVANE 184
OY 161 PGLGLADMSIGVITYILLSGASPLGDTKQETLANITSVSDPDEEFSHTSELAKDPI 240
|
DB 165 PGLGLADMSIGVITYILLSGASPLGDTKQETLANVSAVNEFEDEFSHTSALAKDPI 244
OY 241 RKLAVETRRKRLTIOBALRHPWI 263
|
DB 245 RRLVKKDPKKRMTIODSLQHPWI 267

RESULT 6

US-08-810-712-10
Sequence 10, Application US/088107126
Patent No. 6160106
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co. LTD
TITLE OF INVENTION: Tumor Suppressor Genes, Proteins Encoded Thereby and
FILE REFERENCE: sequence list
CURRENT APPLICATION NUMBER: US/08/810,712G
EARLIER FILING DATE: 1997-03-03
EARLIER APPLICATION NUMBER: PCT/US94/11598
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO: 10
LENGTH: 1423
TYPE: PRT
ORGANISM: Homo sapiens
US-08-810-712-10

Query Match 80.3%; Score 1079; DB 4; Length 1423;
Best Local Similarity 77.2%; Pred. No. 7.6e-88;
Matches 203; Conservative 39; Mismatches 13; Indels 8; Gaps 1;

OY 1 YDIGELSGGQFAIVKCKREKSTGLEVAAKFTKKRQSRASRGVSREELEREVSILROYL 60
|||
DB 13 YDTGELSGGQFAIVKCKREKSTGLQYPAKFKKRTKSSRGVSREREDEVSILKEIQ 72
OY 61 HHNVITLHDVYENRDTDVHILELVSGGELDFDLAOKESLSEBEATSFIIQIIDGVNYLHT 120
|
DB 73 HPNVITLHEVYENKKTQVILILELVAGGELDFDLAOKESLSEBEATFELKQIINGVYLLHS 132
OY 121 KKAIAFDLKPENIMLLDKNIPPIPHIKLIDFGLAHEIEDGVEPKNIFGTFEFAPELVANE 180
|
DB 133 LQIAHFDLKPENIMLLDRNVKPKRIKIDF-----GNEPKNIFGTFEFAPELVANE 184
OY 161 PGLGLADMSIGVITYILLSGASPLGDTKQETLANITSVSDPDEEFSHTSELAKDPI 240
|

DB 185 PGLGLADMSIGVITYILLSGASPLGDTKQETLANVSAVNEFEDEFSHTSALAKDPI 244
OY 241 RKLAVETRRKRLTIOBALRHPWI 263
|
DB 245 RRLVKKDPKKRMTIODSLQHPWI 267

RESULT 7

US-07-857-224B-23
Sequence 23, Application US/07857224B
Patent No. 5958784
GENERAL INFORMATION:

APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
CITY: Zurich
STATE: none
COUNTRY: Switzerland
ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436

PRIOR APPLICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELEPHONE: (International) 41 1 632 2830
TELEFAX: (International) 41 1 262 2437
TELEX: none
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 260
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: protein
ORIGINAL SOURCE:
ORGANISM: chicken
FEATURE: protein kinase; Table 8 Column 25
PUBLICATION INFORMATION:
AUTHORS:
AUTHORS: Hanks, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLE: The protein kinase family
JOURNAL: Science
VOLUME: 241
PAGES: 42-52
DATE: 1988

US-07-857-224B-23
Query Match 48.3%; Score 649; DB 2; Length 260;
Best Local Similarity 47.9%; Pred. No. 1.9e-50;
Matches 126; Conservative 48; Mismatches 81; Indels 8; Gaps 2;

OY 1 YDIGELSGGQFAIVKCKREKSTGLEVAAKFTKKRQSRASRGVSREELEREVSILROYL 60
|
DB 3 YNIEERLGGKGGQVRLVEKKTKGWAKGFKAYSAK-----EKENIRDEISINCLH 56
OY 61 HHNVITLHDVYENRDTDVHILELVSGGELDFDLAOKESLSEBEATSFIIQIIDGVNYLHT 120
|
DB 57 HRLVQCVDAPEKANIIVALEVWSGELFERIIDDFLTERCIRKYMQISEGVEYIHK 116
OY 121 KKAIAFDLKPENIMLLDKNIPPIPHIKLIDFGLAHEIEDGVEPKNIFGTFEFAPELVANE 180
|
DB 117 QGIVHDLKPENIMCNKTI--GTSIKLIDFGLARLESAGSLKVLGTFEFAPELVANE 174

QY 181 PLGLADWMSIGVITVILLGASPLDGTQOETLANITSVSYDDEEFSHSELAKDPI 240
DB 175 PIGETDMSISGVICITVLLSGSLSPKMDNDNEFLANTSAFTWTFDEAFDELSDAKDPI 234
QY 241 RKLIVKTRKRLTIQELRHPWI 263
DB 235 SNLLKKDKMSRLNCTOCLOHPWL 257

RESULT 8

US-07-857-224B-22

Sequence 22, Application US/07857224B

Patent No. 5958784

GENERAL INFORMATION:

APPLICANT: Benner, Steven A.

TITLE OF INVENTION: Predicting folded structures of proteins

NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:

ADDRESSEE: Steven A. Benner

STREET: Hadlaubstrasse 151

CITY: Zurich

STATE: none

COUNTRY: Switzerland

ZIP: (note: this is an international post code) CH-8092

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.0

SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/857,224B

FILING DATE: 03/25/92

CLASSIFICATION: 436

PRIOR APPLICATION DATA: none

TELECOMMUNICATION INFORMATION:

TELEPHONE: (international) 41 1 632 2830

TELEFAX: (international) 41 1 262 2437

TELEX: none

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 261

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

DESCRIPTION: protein

ORIGINAL SOURCE:

ORGANISM: rabbit

FEATURE: Protein kinase; Table 8 Column 24

PUBLICATION INFORMATION:

AUTHORS: Hanks, S. K.

AUTHORS: Quinn, A. M.

AUTHORS: Hunter, T.

TITLE: The protein kinase family

JOURNAL: Science

VOLUME: 241

PAGES: 42-52

DATE: 1988

US-07-857-224B-22

Query Match 42.6%; Score 571.5; DB 2; Length 261;
Best Local Similarity 43.1%; Pred. No. 1.6e-43;
Matches 112; Conservative 54; Mismatches 85; Indels 9; Gaps 3;

QY 5 ELGSGGFAIVKKCREKSTGLVAAFKIKKROSGRASRGVSRSEIEREVSILROYLHNH 64
DB 7 EALGGGFGAVCTCTEKSTGLKAAVYIKQTPK-----DKEMVLEIEVMNQLNHRNL 60
QY 65 ITLHDVYENRTDVVHILELVSGGELDFLAQKE-SLSEEFASFTQOILDGVNYLHTKKI 123
DB 61 IQLYAAIETPIHEIYLFWEYIEGSELFERIVDEVDYHLEVDVWFVRQIDGLIFMKHRY 120

QY 124 AHFLDKPENIMLDKNIPPIHIKIDPGLAHEIDGVEFKNFGTPPEFVAPRIVNEPIG 183
DB 121 LHLDKPENIMLCVNTTQHL--VKIIDFGLARRVNPNEKLVNFGTPEFLSPVAVNDQS 178
QY 184 LEADWMSIGVITVILLGASPLDGTQOETLANITSVSYDDEEFSHSELAKDPIRL 243
DB 179 KDTDMWSLGVITVILLGASPLDGTQOETLANITSVSYDDEEFSHSELAKDPIVNL 238
QY 244 IVKTRKRLTIQELRHPWI 263
DB 239 IVKEGARRMSAAOCLAHFWL 258

RESULT 9

US-08-713-828-1

Sequence 1, Application US/08713828

Patent No. 5683910

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Goli, Surya K.

TITLE OF INVENTION: NOVEL HUMAN PHOSPHORYLASE

TITLE OF INVENTION: KINASE GAMMA SUBUNIT

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: U.S.

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: diskette

COMPUTER: IBM compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/713,828

FILING DATE: Filed Herewith

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0068 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-845-4166

TELEFAX: 415-855-0555

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 307 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

LIBRARY:

CLONE: Consensus

US-08-713-828-1

Query Match 40.4%; Score 542.5; DB 1; Length 307;
Best Local Similarity 44.6%; Pred. No. 7.5e-41;
Matches 103; Conservative 58; Mismatches 63; Indels 7; Gaps 5;

QY 38 RASHRGVS-REETIEREVSILROYLHNH--VITLHDVYENRTDVVHILELVSGGELDFD 92
DB 2 RKRKGGDCRMELIHETAVL-ELAODNPVYINHEVYETASEMITVLEYAAGEIFDQCV 60
QY 93 LAQKESLSEEFASFTQOILDGVNYLHTKKIAHFDLKPENIMLDKNIPPIHIKIDPGL 152
DB 61 ANREDARERKDVORLMOQLLEGVHFLTRDYNHLDLKPQULLTSSS-PLGDIKIYDFGL 119
QY 153 AHEIEDGVEFKNFGTPPEFVAPRIVNEPIGLADWMSIGVITVILLGASPLDGTQKE 212

Db 120 SRLKNSSEELREIMGTPEYVAPETLSYDPISMATDMWSIGVLTGYMLTGISPLGNDKOE 179

QY 213 TLANTISVSYDDEFFSHTSELAKDFIRKLKLVKETRKRLTIOEALRHPWI 263

Db 180 TFLNISQMLSYSEEFVLSASAVDFIRTLVKKPEDRATAECLKHPWL 230

RESULT 10

US-08-919-627-1

; Sequence 1, Application US/08919627

; Patent No. 5833981

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Goll, Surya K.

; TITLE OF INVENTION: NOVEL HUMAN PHOSPHORYLASE

; TITLE OF INVENTION: KINASE GAMMA SUBUNIT

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/919,627

; FILING DATE: August 28, 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/713,828

; FILING DATE: September 13, 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0068-1 DIV

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-855-0555

; TELEFAX: 650-845-4166

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 307 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; IMMEDIATE SOURCE:

; LIBRARY:

; CLONE: Consensus

US-08-919-627-1

Query Match 40.4%; Score 542.5; DB 2; Length 307;
Best Local Similarity 44.6%; Pred. No. 7.5e-41;
Matches 103; Conservative 58; Mismatches 63; Indels 7; Gaps 5;

QY 38 RASRRCVS-REIEREVSILROYLVHN--VITLHDYENRTDVNHLIELVSGGELPD--F 92

Db 2 RRRKQDCRMELIHEIYAVL-ELAQDPWYINLHEVEYETASEMILVLEVAAGEITDQCV 60

QY 93 LAOKESLSESEATSFIKOILDGVNYLTKKIAHFDLKPENIMLDKNIPRIKILDFGL 152

Db 61 ANEDAFKREDVQRLMROILEGVHFLHTRDVNHLDLKPOHILTSSES-PLGDIKIYDFGL 119

QY 153 AHEIDGVEFKNIPTPEYVAPETLSYDPISMATDMWSIGVLTGYMLTGISPLGNDKOE 212

Db 120 SRLKNSSEELREIMGTPEYVAPETLSYDPISMATDMWSIGVLTGYMLTGISPLGNDKOE 179

QY 213 TLANTISVSYDDEFFSHTSELAKDFIRKLKLVKETRKRLTIOEALRHPWI 263

RESULT 12

Db 180 TFLNISQMLSYSEEFVLSASAVDFIRTLVKKPEDRATAECLKHPWL 230

RESULT 11

US-09-096-245-1

; Sequence 1, Application US/09096245

; Patent No. 5977320

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Goll, Surya K.

; TITLE OF INVENTION: NOVEL HUMAN PHOSPHORYLASE

; TITLE OF INVENTION: KINASE GAMMA SUBUNIT

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/096,245

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/713,828

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0068 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 307 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; IMMEDIATE SOURCE:

; LIBRARY:

; CLONE: Consensus

US-09-096-245-1

Query Match 40.4%; Score 542.5; DB 2; Length 307;
Best Local Similarity 44.6%; Pred. No. 7.5e-41;
Matches 103; Conservative 58; Mismatches 63; Indels 7; Gaps 5;

QY 38 RASRRCVS-REIEREVSILROYLVHN--VITLHDYENRTDVNHLIELVSGGELPD--F 92

Db 2 RRRKQDCRMELIHEIYAVL-ELAQDPWYINLHEVEYETASEMILVLEVAAGEITDQCV 60

QY 93 LAOKESLSESEATSFIKOILDGVNYLTKKIAHFDLKPENIMLDKNIPRIKILDFGL 152

Db 61 ANEDAFKREDVQRLMROILEGVHFLHTRDVNHLDLKPOHILTSSES-PLGDIKIYDFGL 119

QY 153 AHEIDGVEFKNIPTPEYVAPETLSYDPISMATDMWSIGVLTGYMLTGISPLGNDKOE 212

Db 120 SRLKNSSEELREIMGTPEYVAPETLSYDPISMATDMWSIGVLTGYMLTGISPLGNDKOE 179

QY 213 TLANTISVSYDDEFFSHTSELAKDFIRKLKLVKETRKRLTIOEALRHPWI 263

Db 180 TFLNISQMLSYSEEFVLSASAVDFIRTLVKKPEDRATAECLKHPWL 230

RESULT 12

US-08-826-267-2


```
Patent No. 6207148
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guebler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272,796
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSNOT06
CLONE: 827431
US-09-272-796-5

Query Match 36.7%; Score 492.5; DB 4; Length 343;
Best Local Similarity 39.6%; Pred. No. 2.5e-36;
Matches 105; Conservative 55; Mismatches 94; Indels 11; Gaps 4;

QY 1 YDIGEELSGGQFAIVKKRREKSTGLEAAKFIKKRQSRASRGVSRREIEREVSIIROYL 60
DB 15 YERERLGSAGSEVVLADQERSAHLVALKCFKKALRG-----KALVNEETAVLRIS 69
QY 61 HHNVITLHDYENRTDVNHLLELVSGGELDFDLAOKESLSEEAATSFIKOILDGVNYLHT 120
DB 70 HPIVVALVEDVHESRSHLYLAMELVTGGELFDRLIMERSGYTEKQASHLVGVGLAVSYLHS 129
QY 121 KTAHFDLAKENIMLDKNIPRIPIKLI--DFGLAHEIEGVEFKNIGTPEYVAPIVN 178
DB 130 LGIVHRLKPENLLYA---TFPDSKIMVSDFGLS-KIQAGNMIGTAGTGPYVAPELLE 185
QY 179 YEPGLLEADMSIGVITYILLSGASPLDGTQKQETLANITSVSDPDPEEFSSHSELA 238
DB 186 QKPYGKAVDVALGVISTYLLCGTPPEYDSDPELSQIIRASTYFDXPIWMDISESGKD 245
QY 239 FIRKLIVKETRRKRLTIOELRHPMI 263
DB 246 FIRHLERDLQKRRFTCOQALRLMI 270
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RESULT 15
US-08-715-568A-1
Sequence 1, Application US/08715568A
Patent No. 5856463
GENERAL INFORMATION:
APPLICANT: Prydz, Hans Peter Blankenborg
APPLICANT: Brede, Gaute
TITLE OF INVENTION: PSKH-1 Ribozymes and uses in Disease
TITLE OF INVENTION: Treatment
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/715,568A
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Foley, Shawn P.
REFERENCE/DOCKET NUMBER: FORSK 3.0-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-715-568A-1

Query Match 36.4%; Score 489.5; DB 2; Length 424;
Best Local Similarity 41.2%; Pred. No. 6e-36;
Matches 110; Conservative 43; Mismatches 101; Indels 13; Gaps 5;

QY 1 YDIGEELSGGQFAIVKKRREKSTGLEAAKFIKKRQSRASRGVSRREIEREVSIIROYL 60
DB 98 YDIKEITGRGSFSAVVAVEHRAHQPYAIAKMIETKY----REG--REVCESELVLRVR 151
QY 61 HHNVITLHDYENRTDVNHLLELVSGGELDFDLAOKESLSEEAATSFIKOILDGVNYLHT 120
DB 152 HANIQVEVEFEOERYVMELATGELFDRIIAKCSFTERDRIYLAQVLDGVRFLHA 211
QY 121 KTAHFDLAKENIMLDKNIPRIPIKLI--DFGLAHEIEGVE--FKNIGTPEYVAPI 176
DB 212 LGITHRLKPENLLYA---PGTDSKITITIDFGLASARKKGDGDLMTTGTPEYIAPV 268
QY 177 VNEPGLLEADMSIGVITYILLSGASPLDGTQKQETLANITSVSDPDPEEFSSHSELA 236
DB 269 LVRRPYNSVDMMALGVIAVITLLSGTWPFEEDDNTRILYROIIRKYSYSGSPMPSVNL 328
QY 237 KDFIRKLIVKETRRKRLTIOELRHPMI 263
DB 329 KDFIDRLITVDPGARMVALQALRHPW 355
```

Search completed: March 26, 2003, 19:11:24
Job time : 13.5538 secs

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Db 193 PGLGADMSIGVITVYLLSGASPLGGETKQETLTNTISAVNYDEDEYFSTSELAQDFI 252

QY 241 RKLIVKTRKRLTIOEALRHPWI 263

Db 253 RRLIVKDKRRRTIQAQLEHSMI 275

RESULT 2

US-09-858-664A-17

Sequence 17, Application US/09858664A

Patent No. US20020072491A1

GENERAL INFORMATION:

APPLICANT: WEI, Ming-Hui, et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

FILE REFERENCE: C1000927-CIP

CURRENT APPLICATION NUMBER: US/09/858,664A

CURRENT FILING DATE: 2001-05-17

PRIOR APPLICATION NUMBER: 09/711,134

PRIOR FILING DATE: 2000-11-11

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 17

LENGTH: 298

TYPE: PRT

ORGANISM: Homo sapiens

US-09-858-664A-17

Query Match 47.4%; Score 636.5; DB 10; Length 298;

Best Local Similarity 47.3%; Pred. No. 7,8e-42;

Matches 125; Conservative 49; Mismatches 81; Indels 9; Gaps 3;

QY 1 YDIGELSGGFATVKKCRKSTGLEAYAKFIKKQSRASRGVSRREIEREVSILROYL 60

Db 7 YDIERLSSGKFGQVRLVEKTRKRWAGKFFKAYSAR-----EKENIQEISTIMNCH 60

QY 61 HHNVITLHDYENRTDVVHILEVSGGELDFDLAKE-SLSEEAATSFIIQIIDGVNYLH 119

Db 61 HPKLVQCVDAFEERKANIVMLEIVSGELFERIIDEFELTERECIKYMQISEGVEYIH 120

QY 120 TKRIAHDLKPNIMLDKNIPPIHKLIDFGLAHEIDGVEKKNIFGTPPEVAPAEIVNY 179

Db 121 KQGIHDLKPNIMCVNKT--GTRIKLIDFGLARLENAGSLKVLFGTPPEVAPAEIVNY 178

QY 180 EPLGLADMSIGVITVYLLSGASPLGGETKQETLTNTISAVNYDEDEYFSTSELAQDF 239

Db 179 EPLSATDMSIGVITVYLLSGASPLGGETKQETLTNTISAVNYDEDEYFSTSELAQDF 238

QY 240 IRKLIVKTRKRLTIOEALRHPWI 263

Db 239 ISNLLKKDKMKNRLDCTOCLQHPWL 262

RESULT 3

US-09-858-664A-18

Sequence 18, Application US/09858664A

Patent No. US20020072491A1

GENERAL INFORMATION:

APPLICANT: WEI, Ming-Hui, et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

FILE REFERENCE: C1000927-CIP

CURRENT APPLICATION NUMBER: US/09/858,664A

CURRENT FILING DATE: 2001-05-17

PRIOR APPLICATION NUMBER: 09/711,134

PRIOR FILING DATE: 2000-11-11

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 18

LENGTH: 508

TYPE: PRT

ORGANISM: Homo sapiens

US-09-858-664A-18

Query Match 47.4%; Score 636.5; DB 10; Length 508;

Best Local Similarity 46.5%; Pred. No. 1.4e-41;

Matches 125; Conservative 49; Mismatches 81; Indels 9; Gaps 3;

QY 1 YDIGELSGGFATVKKCRKSTGLEAYAKFIKKQSRASRGVSRREIEREVSILROYL 60

Db 250 YDIERLSSGKFGQVRLVEKTRKRWAGKFFKAYSAR-----EKENIQEISTIMNCH 303

QY 61 HHNVITLHDYENRTDVVHILEVSGGELDFDLAKE-SLSEEAATSFIIQIIDGVNYLH 119

Db 304 HPKLVQCVDAFEERKANIVMLEIVSGELFERIIDEFELTERECIKYMQISEGVEYIH 363

QY 120 TKRIAHDLKPNIMLDKNIPPIHKLIDFGLAHEIDGVEKKNIFGTPPEVAPAEIVNY 179

Db 364 KQGIHDLKPNIMCVNKT--GTRIKLIDFGLARLENAGSLKVLFGTPPEVAPAEIVNY 421

QY 180 EPLGLADMSIGVITVYLLSGASPLGGETKQETLTNTISAVNYDEDEYFSTSELAQDF 239

Db 422 EPLSATDMSIGVITVYLLSGASPLGGETKQETLTNTISAVNYDEDEYFSTSELAQDF 481

QY 240 IRKLIVKTRKRLTIOEALRHPWI 263

Db 482 ISNLLKKDKMKNRLDCTOCLQHPWL 505

RESULT 4

US-09-940-921B-7

Sequence 7, Application US/09940921B

Patent No. US20020147320A1

GENERAL INFORMATION:

APPLICANT: Fridgley, Carl Johan

APPLICANT: Hilbun, Ertn

APPLICANT: Nepomulchy, Boris

TITLE OF INVENTION: NO. US20020147320A1 Human Kinase Proteins and Polynucleotide

FILE REFERENCE: LEX-0227-USA

CURRENT APPLICATION NUMBER: US/09/940,921B

CURRENT FILING DATE: 2002-05-21

PRIOR APPLICATION NUMBER: US 60/229,280

PRIOR FILING DATE: 2000-08-31

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 7

LENGTH: 388

TYPE: PRT

ORGANISM: homo sapiens

US-09-940-921B-7

Query Match 46.0%; Score 617.5; DB 10; Length 388;

Best Local Similarity 46.5%; Pred. No. 3e-40;

Matches 121; Conservative 53; Mismatches 77; Indels 9; Gaps 3;

QY 5 EELGSGGFATVKKCRKSTGLEAYAKFIKKQSRASRGVSRREIEREVSILROYLHHNV 64

Db 110 EILGSGKFGQVRLVEKTRKRWAGKFFKAYSAR-----DKEVNNELISVMQDQHANL 163

QY 65 ITHDYENRTDVVHILEVSGGELDFDLAKE-SLSEEAATSFIIQIIDGVNYLHKT 123

Db 164 IOLYDAFESNDLVLMVEYVDGELFRIDESYNTLDELPTILFMKQICGIRHMOMYI 223

QY 124 AHFDLKPENIMLDKNIPPIHKLIDFGLAHEIDGVEKKNIFGTPPEVAPAEIVNY 183

Db 224 LHLDLKPNIMCVNKT--AKQIKLIDFGLARRRKPRKLVNGETPEFLAPAEIVNYFVS 281

QY 184 LEADMSIGVITVYLLSGASPLGGETKQETLTNTISAVNYDEDEYFSTSELAQDFIRKL 243

Db 282 FPLDMSIGVITVYLLSGASPLGGETKQETLTNTISAVNYDEDEYFSTSELAQDFIRKL 341

QY 244 LKVEETRRRLTIOEALRHPWI 263

Db 342 LIKEKSMRISASEALKHPWL 361

RESULT 5

US-09-940-921B-9

Sequence 9, Application US/09940921B

Patent No. US20020147320A1

GENERAL INFORMATION:

APPLICANT: Friddele, Carl Johan

APPLICANT: Hildun, Erin

APPLICANT: Nepomilichy, Boris

APPLICANT: Hu, Yi

TITLE OF INVENTION: No. US20020147320A1el Human Kinase Proteins and Polynucleotides H

FILE REFERENCE: LEX-0227-USA

CURRENT APPLICATION NUMBER: US/09/940,921B

PRIOR FILING DATE: 2002-05-21

PRIOR APPLICATION NUMBER: US 60/229,280

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 9

LENGTH: 398

TYPE: PRT

ORGANISM: homo sapiens

US-09-940-921B-9

Query Match

Best Local Similarity 46.0%; Score 617.5; DB 10; Length 398;

Best Local Similarity 46.5%; Pred. No. 3.1e-40;

Matches 121; Conservative 53; Mismatches 77; Indels 9; Gaps 3;

Db 5 BELGSGQFAIVKKCRKSTGLEVAAKFIKKRQSRASRGVSRREIEREVSILROVLHHNV 64

110 ELTGGRFGQVHKCEETATGLAKAIIITRGK-----DKEEVNEISVMQOLDHANL 163

65 ITLHDVYENRTDVVHILELVSGGELFD-FLAOKESLSEBEATSFIOIIDGVNYLTHTKKI 123

164 IOLYDAFESKNDIVLMEVYDGGELFDRIIDESYNLTDLTILFMKICEGIIHMHQMYI 223

124 AHFDLKPENIMLDKNIPRPHIKLIDFGLAHEIEDGVFEKRNIFGTPEFAVAPETVNEPLG 183

224 LHLDRKPEMLICVNRD--AKQIKIIDFGIARRKPREKIKVNGCTPEFLAPEVNVYDFVS 281

184 LEADMMISVITYIILSGASPLGDTKQETLANITSVSYDFDEEFSHSSELAKDPIRKL 243

282 EFTDMNSVIVAMLLSGSPFLGDNDATLNNIILACRWLEDEEDODISEAKETISKL 341

Db 244 LVKETRRKRLTIOEALRHPMI 263

342 LIKEKSMRISASEALKHPWL 361

RESULT 6

US-09-925-300-1442

Sequence 1442, Application US/09925300

Patent No. US20020151681A1

GENERAL INFORMATION:

APPLICANT: Craig Rosen,

APPLICANT: Steve Ruben

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA101

CURRENT APPLICATION NUMBER: US/09/925,300

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05988

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270

NUMBER OF SEQ ID NOS: 1890

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1442

LENGTH: 839

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (291)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (295)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (683)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-925-300-1442

Query Match

Best Local Similarity 45.5%; Score 611.5; DB 10; Length 839;

Best Local Similarity 47.7%; Pred. No. 2.1e-39;

Matches 123; Conservative 46; Mismatches 80; Indels 9; Gaps 3;

Db 1 YDIGELSGQFAIVKKCRKSTGLEVAAKFIKKRQSRASRGVSRREIEREVSILROVL 60

585 YDIEERLGSQKFGQVFRVLEKTRKRWAGKFFKAYSAK-----EKENIQEISIMNCLH 638

61 HHNVITLHDVYENRTDVVHILELVSGGELFDPLAOKE-SLSEBEATSFIOIIDGVNYLT 119

639 HPKLVQCVDAFEEKANIVMLVLEIVSGGELFERIIDEDFELTEREKIKYMQISEGVEYIH 698

120 TKRIAHFDLKPENIMLDKNIPRPHIKLIDFGLAHEIEDGVFEKRNIFGTPEFAVAPETV 179

699 KQGVHLDLKPENIMCVNKT--GTRIKLIDFGLARRLENAGSLKVLGTPEFAVAPETV 756

180 EPLGLEADMSIGVITYIILSGASPLGDTKQETLANITSVSYDFDEEFSHSSELAKE 239

757 EPIGATDMNSIGVICIIVLGSGLSPFGMDNDETLANVTSATWDFDEADEISDAKDF 816

Db 240 IRLKLVKETRRKRLTIOEA 257

817 ISNLLKMDKMRNLDCTHA 834

RESULT 7

US-09-797-039-8

Sequence 8, Application US/09797039

Patent No. US20020042099A1

GENERAL INFORMATION:

APPLICANT: Olandt, Peter J,

APPLICANT: Kapeller-Libermann, Rosana

TITLE OF INVENTION: 2504, 15977, AND 14760, NOVEL PROTEIN

TITLE OF INVENTION: KINASE FAMILY MEMBERS AND USES THEREFOR

FILE REFERENCE: 10448-017001

CURRENT APPLICATION NUMBER: US/09/797,039

CURRENT FILING DATE: 2001-02-28

PRIOR APPLICATION NUMBER: US 60/186,061

PRIOR FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 8

LENGTH: 596

TYPE: PRT

ORGANISM: Homo sapiens

US-09-797-039-8

Query Match

Best Local Similarity 42.4%; Score 569.5; DB 10; Length 596;

Best Local Similarity 42.7%; Pred. No. 2.5e-36;

Matches 111; Conservative 55; Mismatches 85; Indels 9; Gaps 3;

Db 5 BELGSGQFAIVKKCRKSTGLEVAAKFIKKRQSRASRGVSRREIEREVSILROVLHHNV 64

289 EALGGGKFGAVCTCMERATGLAKAVIKRQTER-----DKREVLLIEIVMQLNHRNL 342

65 ITLHDVYENRTDVVHILELVSGGELFDPLAOKE-SLSEBEATSFIOIIDGVNYLTHTKKI 123

343 IOLYAEITPHEIVLMEVYEGGELFERIYDDEHILTEVDTPVFRQICGILFPMHMRV 402

124 AHFDLKPENIMLDKNIPRPHIKLIDFGLAHEIEDGVFEKRNIFGTPEFAVAPETVNEPLG 183

403 LHLDRKPEMLICVNTTGH--VKIIDGLARRVNPNEKLVNNGTPEFLAPEVNVYDFVS 460

RESULT 11

US-09-858-664A-13
; Sequence 13, Application US/09858664A
; Patent No. US20020072491A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui, et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEROOF
; FILE REFERENCE: CLO00927-CIP
; CURRENT APPLICATION NUMBER: US/09/858,664A
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/711,134
; PRIOR FILING DATE: 2000-11-11
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-858-664A-13

Query Match 37.2%; Score 500; DB 10; Length 414;
Best Local Similarity 38.8%; Pred. No. 3.6e-31;
Matches 100; Conservative 57; Mismatches 93; Indels 8; Gaps 2;

QY 6 ELGSGQFAIVKCKREKSTGLEVAFAKFIKKRQSRASRGVSRREIEREVSILRQVLHNVY 65
DB 118 ELGRGFVSVKCKDOKGTRAVATKFNKKL-----MKRQVTHELILQSLQHLPLV 170
QY 66 TLHDVYENRTDVVHILEVSGELFDLQAKSLSSEEAFTSPIKQILDGVNVLHKKIAH 125
DB 171 GLDTEFPTSYLVLEMDQGRLLDCVVRMSLIEGKIRAHGELVAVRYLHNCRIAH 230
QY 126 FDLKPEINMLL--DKNIPRIPIKILDFGLAHEIDGVEFKNIFGPPFVAREIYVPEPLGE 185
DB 231 LDKPEINL--LVDESLAKPIKILADGEDAVQVLTNTYTHQLGPEFAPEIILGNFVSIL 289
QY 186 ADMWSIGVITYILLGSGAPFLDGTQKQETLANITSVSYDEDEFFSHTSELAKDFIRKLV 245
DB 290 SDTWSVGVLTIVLLGSPFLDSVETCLNICRDLDFSPDDYFKVSGKAKGEVCFLLQ 349
QY 246 KETRRKRLTIOEALRHPI 263
DB 350 EDPARRPSAALALQEQWL 367

RESULT 12

US-09-935-464-3
; Sequence 3, Application US/09935464
; Publication No. US20030027153A1
; GENERAL INFORMATION:
; APPLICANT: Meyer, Joanne
; APPLICANT: Barrington-Martin, Rory
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIA
; TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
; FILE REFERENCE: 3322/14702 US1
; CURRENT APPLICATION NUMBER: US/09/935,464
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US 09/757,300
; PRIOR FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-464-3

Query Match 37.2%; Score 500; DB 9; Length 460;

Best Local Similarity 41.4%; Pred. No. 4.1e-31;
Matches 108; Conservative 51; Mismatches 90; Indels 12; Gaps 5;

QY 5 EEIGSGQFAIVKCKREKSTGLEVAFAKFIKKRQSRASRGVSRREIEREVSILRQVLHNVY 64
DB 27 EVLGSGAFSEVFLVKQRLGKLFALCKIKK--SPARR---DSSLNEIATLKKIKHENY 80
QY 65 ITLHDVYENRTDVVHILEVSGELFDLQAKSLSSEEAFTSPIKQILDGVNVLHKKIAH 124
DB 81 VTLEDIYESTHYLVLMQVLSGGEFLDRLIERGVYTEKDSLVIOQVLSAVKYLHENGIV 140
QY 125 HFDLKEINMLL--DKNIPRIPIKILDFGLAHEIDGVEFKNIFGPPFVAREIYVPEPL 182
DB 141 HRLKPEINLLYLPREN---SKIMTDFGLSKMEQNGI--MSTACGTPGYAVPEVLAQKPY 196
QY 183 GLEADMSIGVITYILLGSGAPFLDGTQKQETLANITSVSYDEDEFFSHTSELAKDFIRK 242
DB 197 SKAVDCMSIGVITYILLGVPPEYEEFTESKLFKIKEGYEFESPPMDISSESADKFICH 256
QY 243 LKVKETRRKRLTIOEALRHPI 263
DB 257 LLEKDPNERYTECKALSHPI 277

RESULT 13

US-09-935-464-5
; Sequence 5, Application US/09935464
; Publication No. US20030027153A1
; GENERAL INFORMATION:
; APPLICANT: Meyer, Joanne
; APPLICANT: Barrington-Martin, Rory
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIA
; TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
; FILE REFERENCE: 3322/14702 US1
; CURRENT APPLICATION NUMBER: US/09/935,464
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US 09/757,300
; PRIOR FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-464-5

Query Match 37.2%; Score 500; DB 9; Length 476;
Best Local Similarity 41.4%; Pred. No. 4.2e-31;
Matches 108; Conservative 51; Mismatches 90; Indels 12; Gaps 5;

QY 5 EEIGSGQFAIVKCKREKSTGLEVAFAKFIKKRQSRASRGVSRREIEREVSILRQVLHNVY 64
DB 27 EVLGSGAFSEVFLVKQRLGKLFALCKIKK--SPARR---DSSLNEIATLKKIKHENY 80
QY 65 ITLHDVYENRTDVVHILEVSGELFDLQAKSLSSEEAFTSPIKQILDGVNVLHKKIAH 124
DB 81 VTLEDIYESTHYLVLMQVLSGGEFLDRLIERGVYTEKDSLVIOQVLSAVKYLHENGIV 140
QY 125 HFDLKEINMLL--DKNIPRIPIKILDFGLAHEIDGVEFKNIFGPPFVAREIYVPEPL 182
DB 141 HRLKPEINLLYLPREN---SKIMTDFGLSKMEQNGI--MSTACGTPGYAVPEVLAQKPY 196
QY 183 GLEADMSIGVITYILLGSGAPFLDGTQKQETLANITSVSYDEDEFFSHTSELAKDFIRK 242
DB 197 SKAVDCMSIGVITYILLGVPPEYEEFTESKLFKIKEGYEFESPPMDISSESADKFICH 256
QY 243 LKVKETRRKRLTIOEALRHPI 263
DB 257 LLEKDPNERYTECKALSHPI 277

RESULT 14

